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<110> Crane, Edmund H. III
      Rice, Douglas A.

<120> Maize NPR1 Polynucleotides and Methods
  of Use

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Tyr Leu Ser Asn Gly Ser Ser Pro Cys Ser Val Ala Leu Pro Pro Pro
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ggg ccg ccc cag act ccc ccg ttg cct gcc ggc cag ggg tgg ggt ggt   204
Gly Pro Pro Gln Thr Pro Pro Leu Pro Ala Gly Gln Gly Trp Gly Gly
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gga gtc gct gcc gca ggg agc gga ggc agc gtg gag gcc gtg agc ctg   252
Gly Val Ala Ala Ala Gly Ser Gly Gly Ser Val Glu Ala Val Ser Leu
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ctc ttc gcc gct cgc ggc cgc gca ggg gca gcg cgc ggt gat gcg gcc        444
Leu Phe Ala Ala Arg Gly Arg Ala Gly Ala Ala Arg Gly Asp Ala Ala
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gcc ggc gcc gga gta gcc gcg gag ggg gct gcc agt gga agg ccg cgg        492
Ala Gly Ala Gly Val Ala Ala Glu Gly Ala Ala Ser Gly Arg Pro Arg
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Tyr Lys Met Glu Asp Leu Val Pro Ala Gly Arg Val Gly Arg Glu Ala
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ccg gtc gac gtg gtg tct tgt gct gac cca gtg tgc cat cac gat tcg        636
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Cys Pro Pro Ala Ile Arg Ser Ala Val Glu Leu Met Tyr Ala Ala Cys
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Asn Phe Val Asp Lys Thr Leu Val Glu Asp Val Ile Pro Ile Leu Glu
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agg att gct aga tca gat ctc gac gat ata tct ttg gat aag gag ctc        876
Arg Ile Ala Arg Ser Asp Leu Asp Asp Ile Ser Leu Asp Lys Glu Leu
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cct cca gaa gca gtt gat gag ata aaa aat ttg cgc aag aag tca caa        924
Pro Pro Glu Ala Val Asp Glu Ile Lys Asn Leu Arg Lys Lys Ser Gln
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act gct gat ggt gat acg ttc att tcg gac cct gtg cat gag aaa aga        972
Thr Ala Asp Gly Asp Thr Phe Ile Ser Asp Pro Val His Glu Lys Arg
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gtc aga aga atc cac agg gca ctt gac tct gat gat gtt gag ctt gtg       1020
Val Arg Arg Ile His Arg Ala Leu Asp Ser Asp Asp Val Glu Leu Val
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aag ttg ctt ctt aat gag tcc gac atc aca tta gat gat gcc aac gca       1068
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aca gca ctc cac ttg gct gct atg agg aga gaa cca gct ata atc atg   1212
Thr Ala Leu His Leu Ala Ala Met Arg Arg Glu Pro Ala Ile Ile Met
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agg agc gca att ggt att tgt cgg agg tta aca aga gca aaa gac tac   1308
Arg Ser Ala Ile Gly Ile Cys Arg Arg Leu Thr Arg Ala Lys Asp Tyr
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aat aca aag atg gag cag ggt caa gaa tca aat aaa gat agg ctg tgt   1356
Asn Thr Lys Met Glu Gln Gly Gln Glu Ser Asn Lys Asp Arg Leu Cys
415                    420                    425                    430

ata gat att cta gag agg gag atg atg cgg aat cct atg gcg gtg gaa   1404
Ile Asp Ile Leu Glu Arg Glu Met Met Arg Asn Pro Met Ala Val Glu
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gat gcc gtc acc tcg cct ttg ttg gca gat gat ctt cac atg aag ctt   1452
Asp Ala Val Thr Ser Pro Leu Leu Ala Asp Asp Leu His Met Lys Leu
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Phe Gly Gly Ile Val Ala Val Ala Ala Ser Thr Ser Gly Lys Leu Arg
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gag gtg gac ctt aat gag acg cca gtg aca caa aac aaa agg ctc cgt   1644
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Ser Arg Val Asp Ala Leu Met Lys Thr Val Glu Leu Gly Arg Arg Tyr
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Phe Pro Asn Cys Ser Gln Val Leu Asp Lys Phe Leu Glu Asp Asp Leu
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Pro Glu Gly Leu Asp Gln Phe Tyr Leu Gln Arg Gly Thr Ala Asp Glu
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cag aag gtg aag agg atg cgc ttc tgc gag ctg aaa gag gac gtg ctg   1836
Gln Lys Val Lys Arg Met Arg Phe Cys Glu Leu Lys Glu Asp Val Leu
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Ser Asp Ala Asp Val Asp Val Pro Asp Gly Gly Pro Pro Val Pro Ile
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Ala Phe Leu Gly Tyr Leu Tyr Thr Gly Lys Leu Arg Pro Ala Pro Val
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<210> 4
<211> 621
<212> PRT
<213> Zea mays

<400> 4

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Pro Gln Thr Pro Pro Leu Pro Ala Gly Gln Gly Trp Gly Gly Gly Val
        35                  40                  45
Ala Ala Ala Gly Ser Gly Gly Ser Val Glu Ala Val Ser Leu Asn Arg
    50                  55                  60
Leu Ser Lys Asn Leu Glu Arg Leu Leu Leu Asp Pro Asp Leu Asp Cys
65                  70                  75                  80
Ser Asp Ala Asp Val Asp Val Pro Asp Gly Gly Pro Pro Val Pro Ile
                85                  90                  95
His Arg Cys Ile Leu Ala Ala Arg Ser Asp Phe Phe Tyr Asp Leu Phe
            100                 105                 110
Ala Ala Arg Gly Arg Ala Gly Ala Ala Arg Gly Asp Ala Ala Ala Gly
        115                 120                 125
Ala Gly Val Ala Ala Glu Gly Ala Ala Ser Gly Arg Pro Arg Tyr Lys
    130                 135                 140
Met Glu Asp Leu Val Pro Ala Gly Arg Val Gly Arg Glu Ala Phe Gln
145                 150                 155                 160
Ala Phe Leu Gly Tyr Leu Tyr Thr Gly Lys Leu Arg Pro Ala Pro Val
                165                 170                 175
Asp Val Val Ser Cys Ala Asp Pro Val Cys His His Asp Ser Cys Pro
                180                 185                 190
Pro Ala Ile Arg Ser Ala Val Glu Leu Met Tyr Ala Ala Cys Thr Phe
            195                 200                 205
Lys Ile Pro Glu Leu Thr Ser Leu Phe Gln Arg Arg Leu Leu Asn Phe
    210                 215                 220
Val Asp Lys Thr Leu Val Glu Asp Val Ile Pro Ile Leu Glu Val Ala
225                 230                 235                 240
Ser His Ser Gly Leu Thr Gln Val Ile Asp Lys Cys Ile Gln Arg Ile
                245                 250                 255
Ala Arg Ser Asp Leu Asp Asp Ile Ser Leu Asp Lys Glu Leu Pro Pro
            260                 265                 270
Glu Ala Val Asp Glu Ile Lys Asn Leu Arg Lys Lys Ser Gln Thr Ala
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               275              ·         ·    280                        285
Asp Gly Asp Thr Phe Ile Ser Asp Pro Val His Glu Lys Arg Val Arg
    290                      295                  300
Arg Ile His Arg Ala Leu Asp Ser Asp Asp Val Glu Leu Val Lys Leu
305                      310                  315                  320
Leu Leu Asn Glu Ser Asp Ile Thr Leu·Asp Asp Ala Asn Ala Leu His
                325                  330                      335
Tyr Ala Ala Ser Tyr Cys Asp Pro Lys Val Val Ser Glu Leu Leu Asp
            340                  345                  350
Leu Ala Met Ala Asn Leu Asn Leu Lys Asn Ser Arg Gly Tyr Thr Ala
            355              ·        360                  365
Leu His Leu Ala Ala Met Arg Arg Glu Pro Ala Ile Ile Met Cys Leu
        370                  375                  380
Leu Asn Lys Gly Ala Asn Val Ser Gln Leu Thr Ala Asp Gly Arg Ser
385                      390                  395                  400
Ala Ile Gly Ile Cys Arg Arg Leu Thr Arg Ala Lys Asp Tyr Asn Thr
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Lys Met Glu Gln Gly Gln Glu Ser Asn Lys Asp Arg Leu Cys Ile Asp
            420                  425                  430
Ile Leu Glu Arg Glu Met Met Arg Asn Pro Met Ala Val Glu Asp Ala
            435                  440                  445
Val Thr Ser Pro Leu Leu Ala Asp Asp Leu His Met Lys Leu Leu Tyr
        450                  455                  460
Leu Glu Asn Arg Val Ala Phe Ala Arg Leu Phe Phe Pro Ala Glu Ala
465                      470                  475                  480
Lys Val Ala Met Gln Ile Ala Gln Ala Asp Thr Thr Glu Glu Phe Gly
                485                  490                  495
Gly Ile Val Ala Val Ala Ala Ser Thr Ser Gly Lys Leu Arg Glu Val
            500                  505                  510
Asp Leu Asn Glu Thr Pro Val Thr Gln Asn Lys Arg Leu Arg Ser Arg
            515                  520                  525
Val Asp Ala Leu Met Lys Thr Val Glu Leu Gly Arg Arg Tyr Phe Pro
        530                  535                  540
Asn Cys Ser Gln Val Leu Asp Lys Phe Leu Glu Asp Asp Leu Pro Glu
545                      550                  555                  560
Gly Leu Asp Gln Phe Tyr Leu Gln Arg Gly Thr Ala Asp Glu Gln Lys
                565                  570                  575
Val Lys Arg Met Arg Phe Cys Glu Leu Lys Glu Asp Val Leu Lys Ala
            580                  585                  590
Phe Ser Lys Asp Lys Ala Glu Gly Ser Val Phe Ser Gly Leu Ser Ser
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<211> 2715
<212> DNA
<213> Zea mays

<220>
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<222> (1)...(2715)

<400> 5
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gacagtcagg tgcccccttc cgaccgttgg ctcggccacg tgtttcgcgc ggatcgcgcg     180
gcagaccgtt ggcccgaccg accgttggct caccggacag tccggtgcac accagacagt     240
ccggtgaatt atagccgtac gccgttaatc·acttcccgag agcagcaagt tcgcctgagc     300
cagcctggcg caccggacac tgtccggtga accaccggac agtccggtgc acccagtcag     360
agctgacttt ggctgaacaa agtcatcttt agttccaact tgattttttcc tgtttccagc     420
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accaaaatac ttagaaatgg cccaagggca catttccctt tcaacagtcc ggtgccacac    600
cggacagtcc ggtgacctct gacttctgtg ttctaacttc tgtcgcggca ctgtttcgca    660
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<210> 6
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Designed oligonucleotide based upon an adaptor
     used for cDNA library construction and poly(dT) to
     remove clones which have a poly(A) tail but no
     cDNA insert.

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tcgacccacg cgtccgaaaa aaaaaaaaaa aaaaaa   36